

FIGURE 1

BEST AVAILABLE COPY

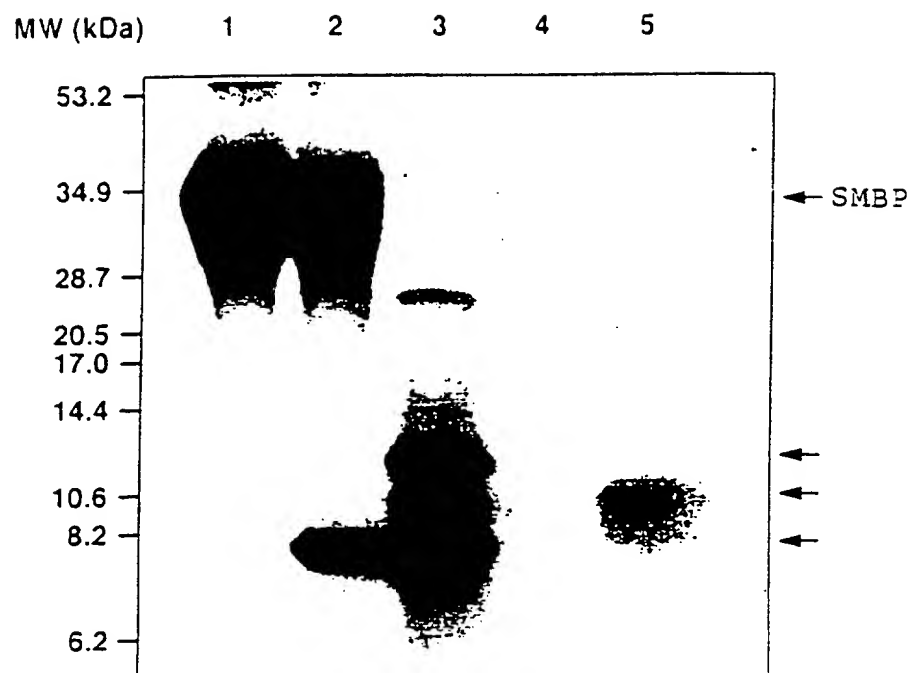


FIGURE 2

BEST AVAILABLE COPY

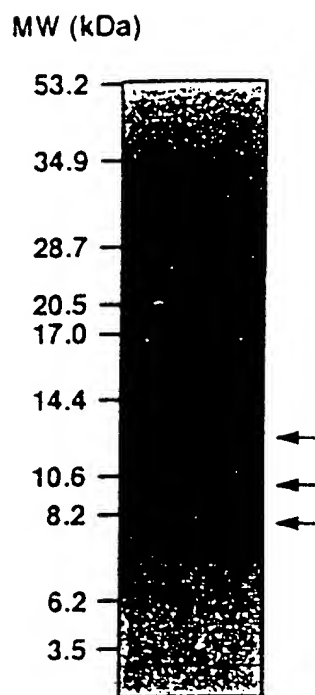


FIGURE 3

BEST AVAILABLE COPY

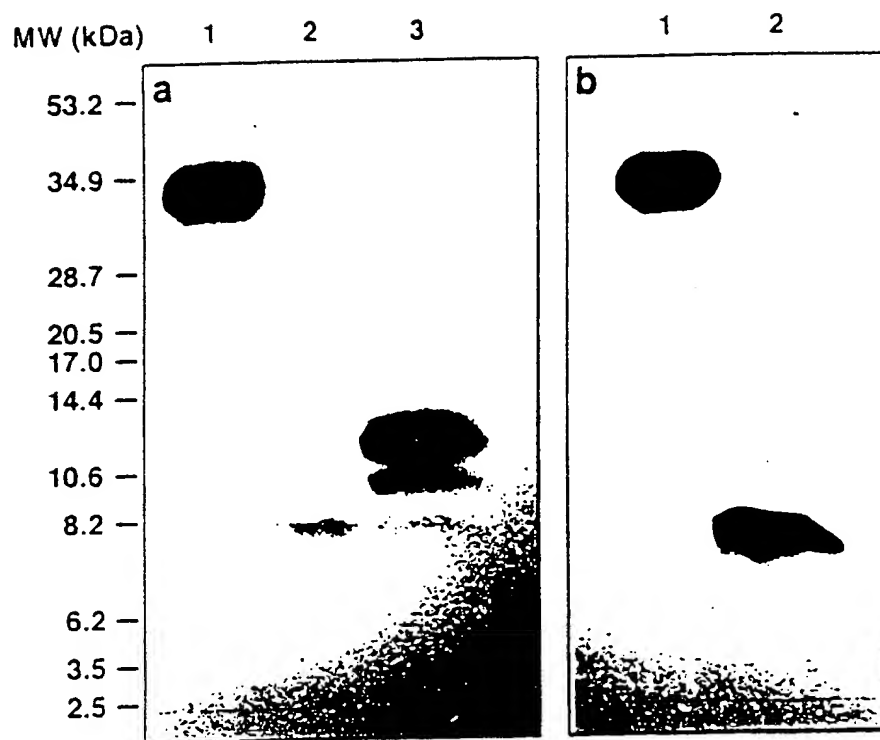


FIGURE 4

BEST AVAILABLE COPY

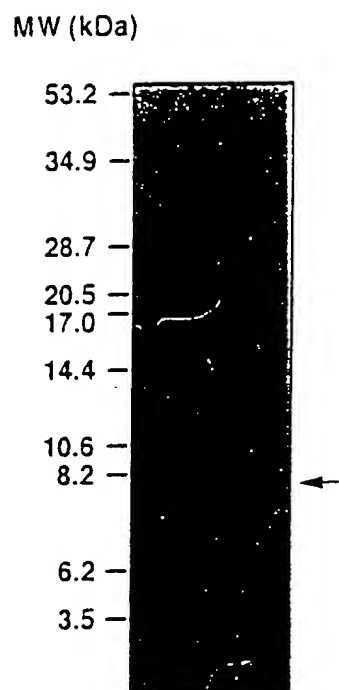


FIGURE 5

BEST AVAILABLE COPY

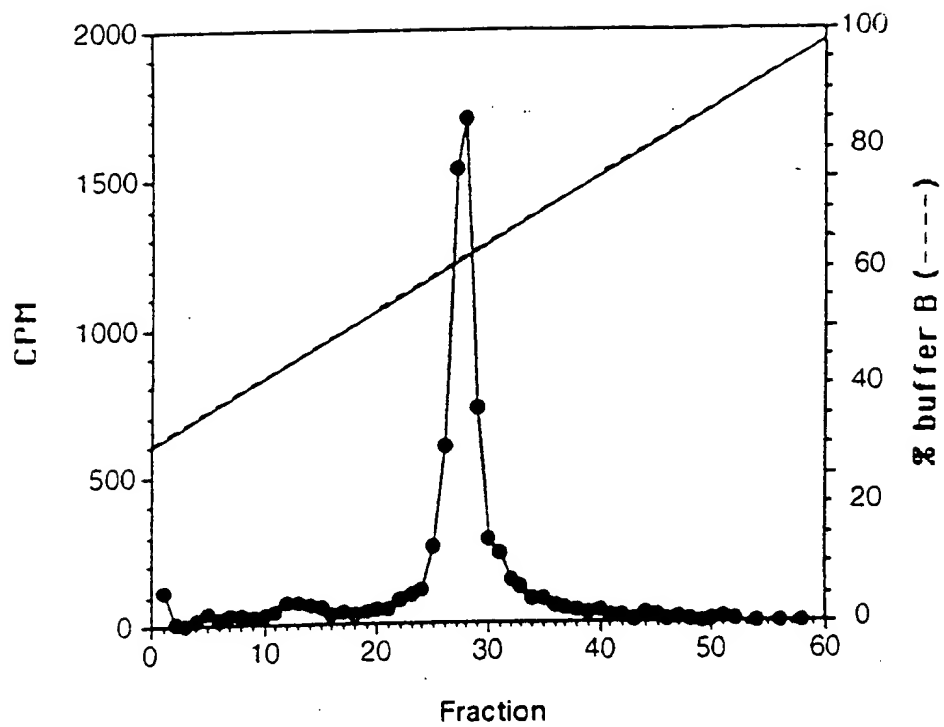


FIGURE 6

BEST AVAILABLE COPY

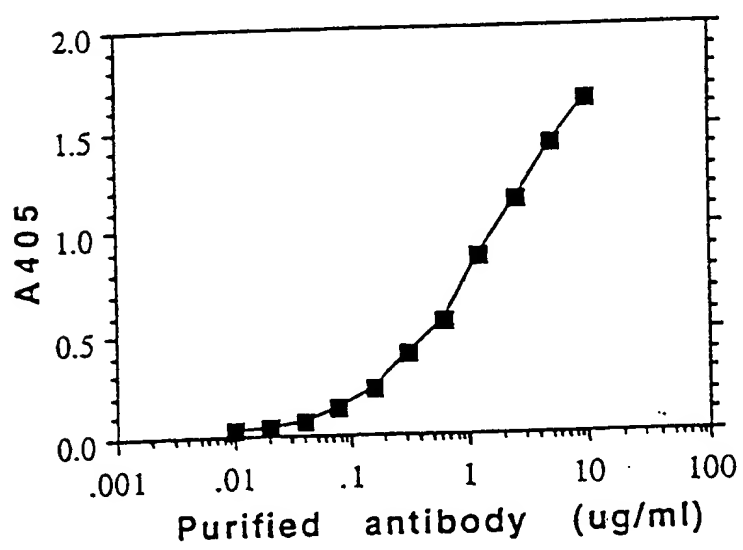
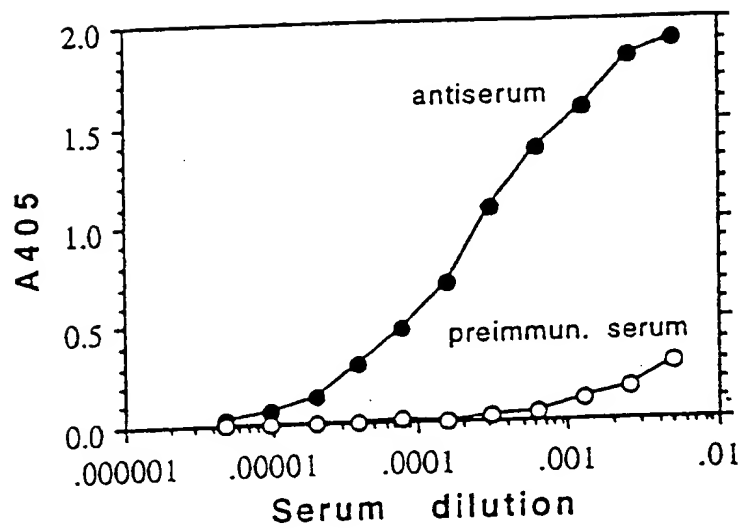


FIGURE 7

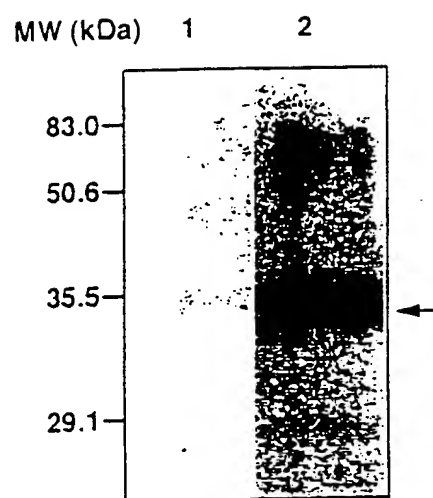


FIGURE 8

BEST AVAILABLE COPY

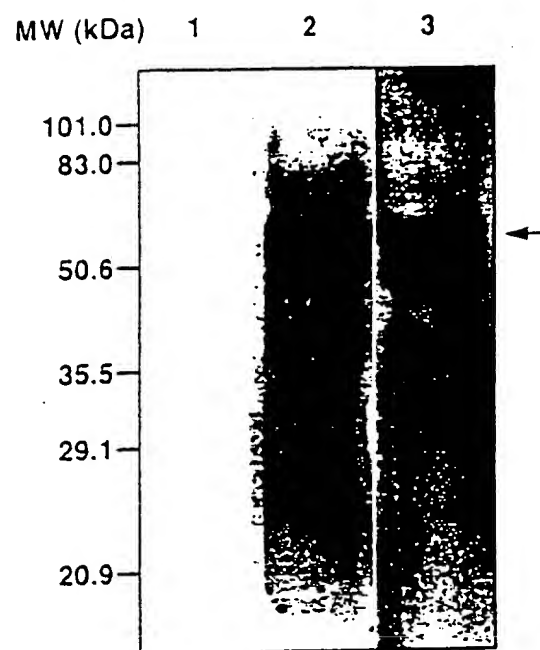


FIGURE 9

BEST AVAILABLE COPY

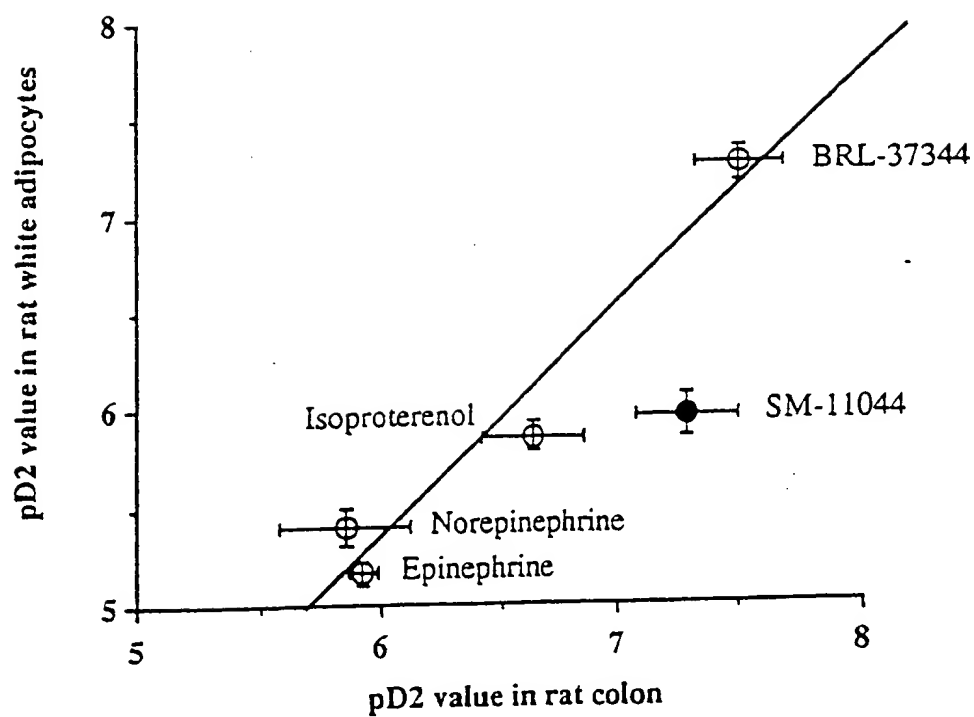


FIGURE 10

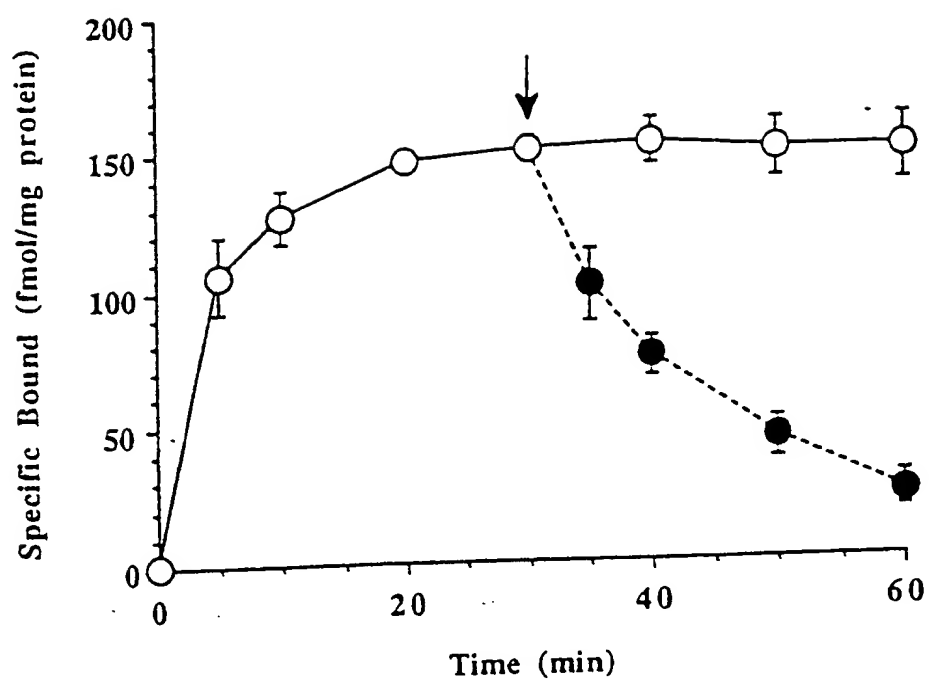


FIGURE 11

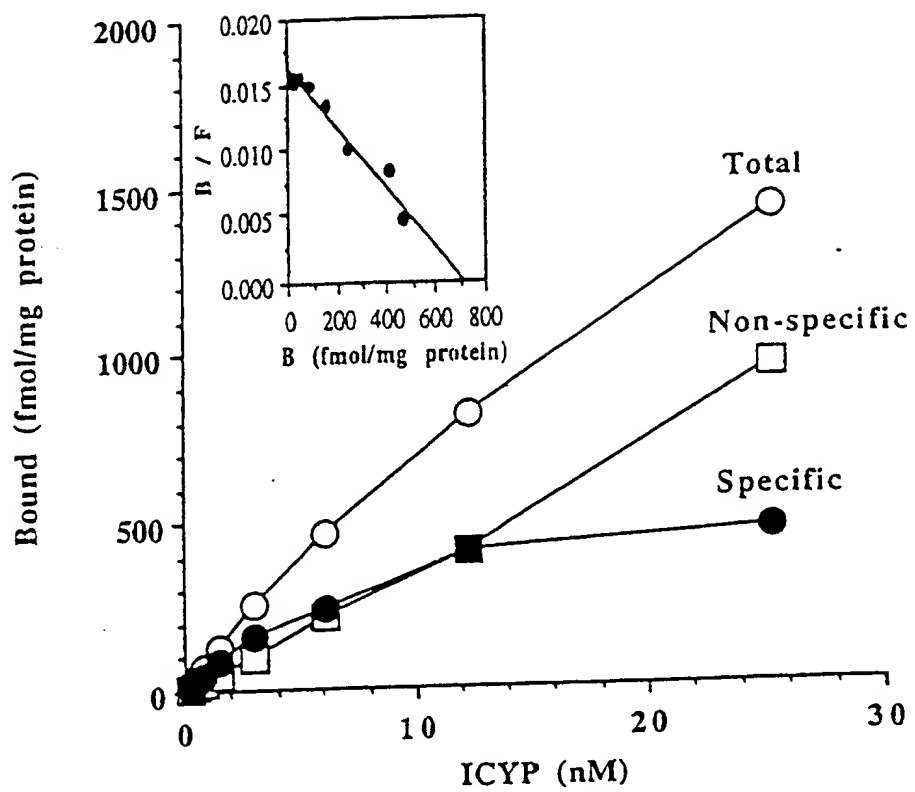


FIGURE 12

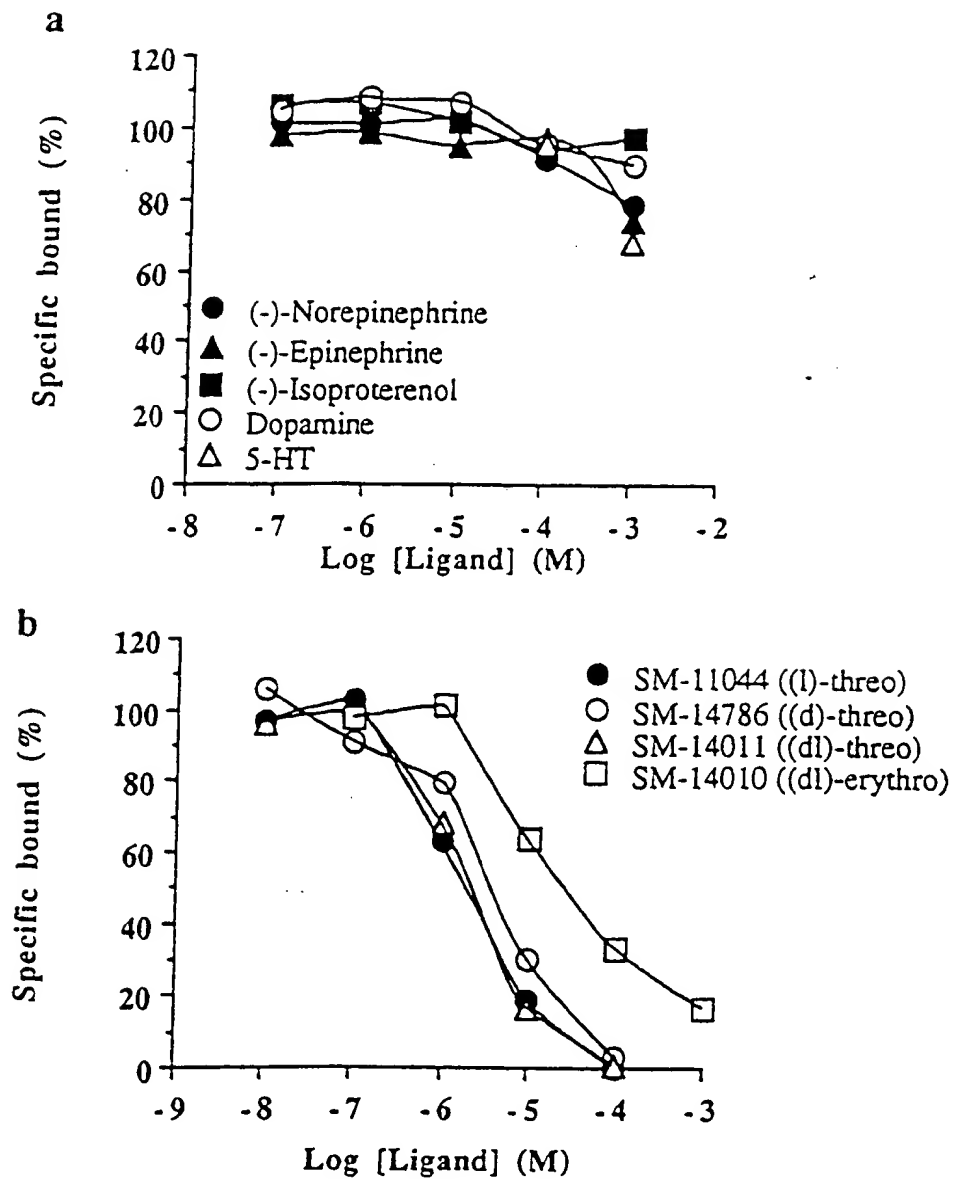


FIGURE 13

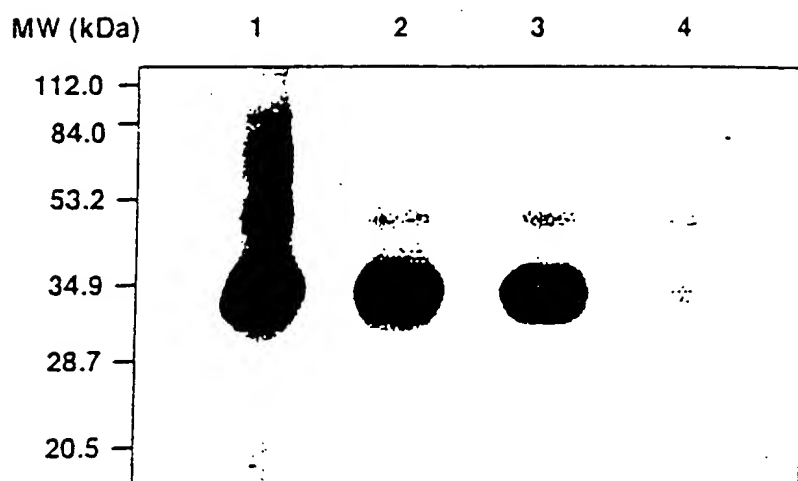


FIGURE 14

BEST AVAILABLE COPY

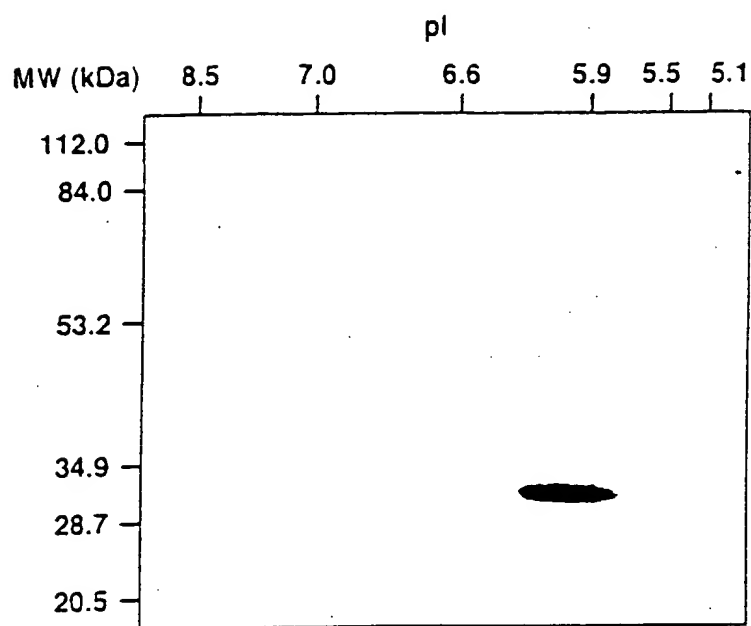


FIGURE 15

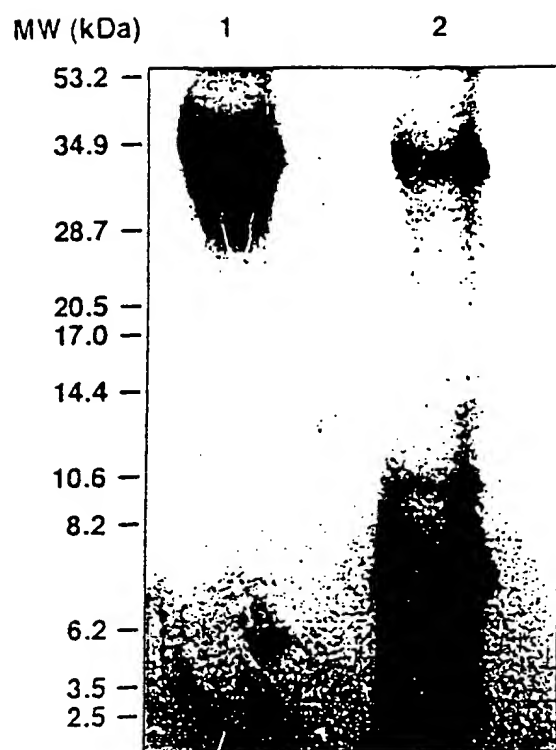


FIGURE 16

BEST AVAILABLE COPY

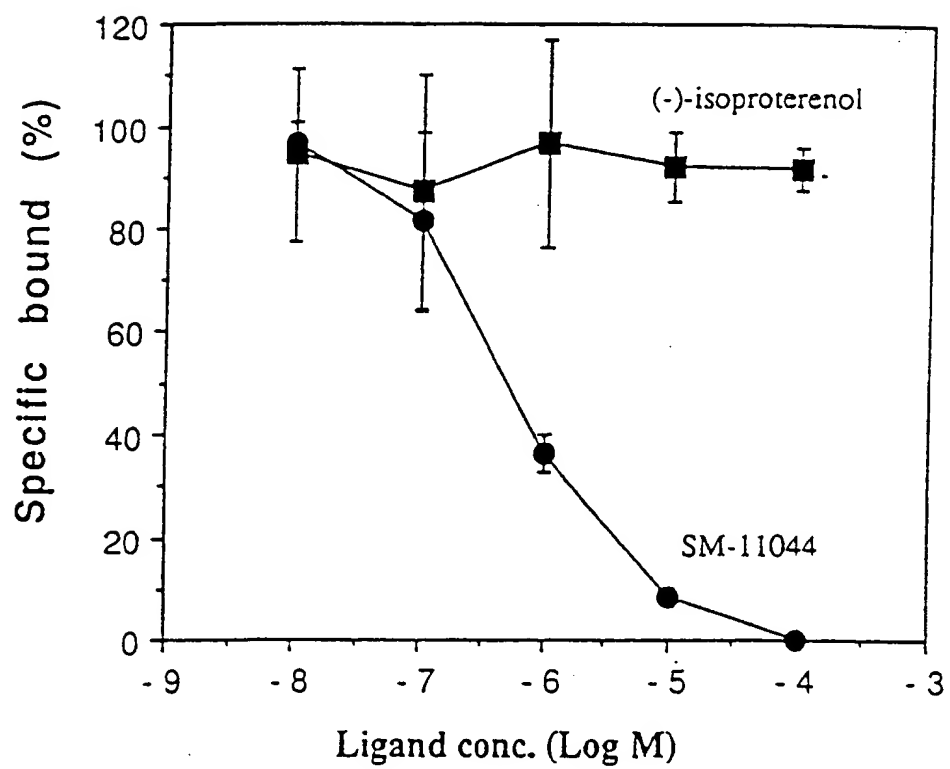
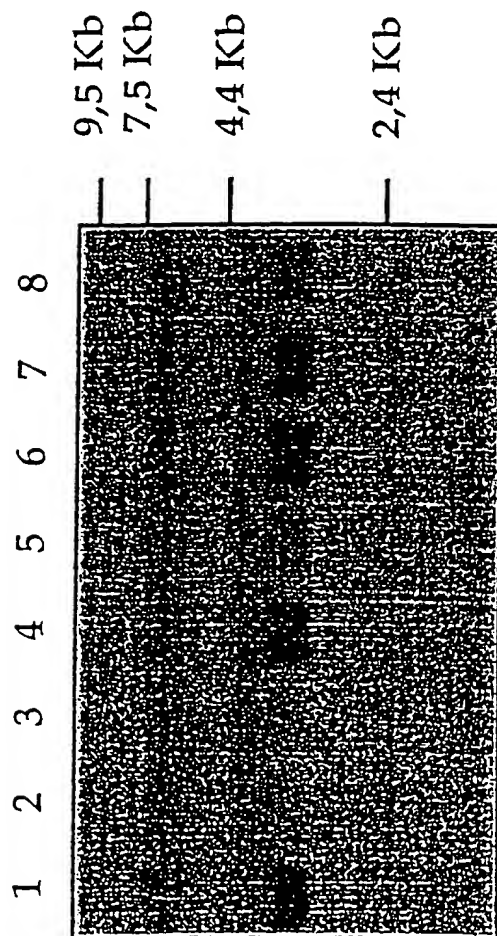


FIGURE 17



- 1 Skeletal muscle
- 2 Uterus (no endometrium)
- 3 Colon (no mucosa)
- 4 Small intestine
- 5 Bladder
- 6 Heart
- 7 Stomach
- 8 Prostate

FIGURE 18.A

BEST AVAILABLE COPY

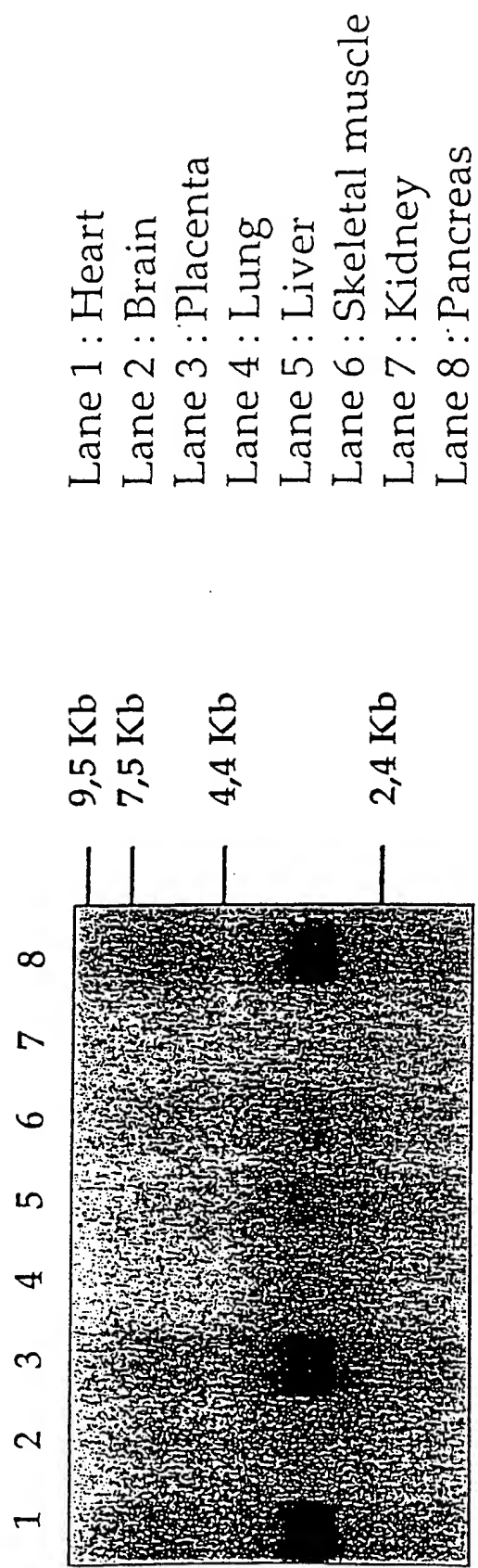


FIGURE 18.B

BEST AVAILABLE COPY

Fig. 19 A

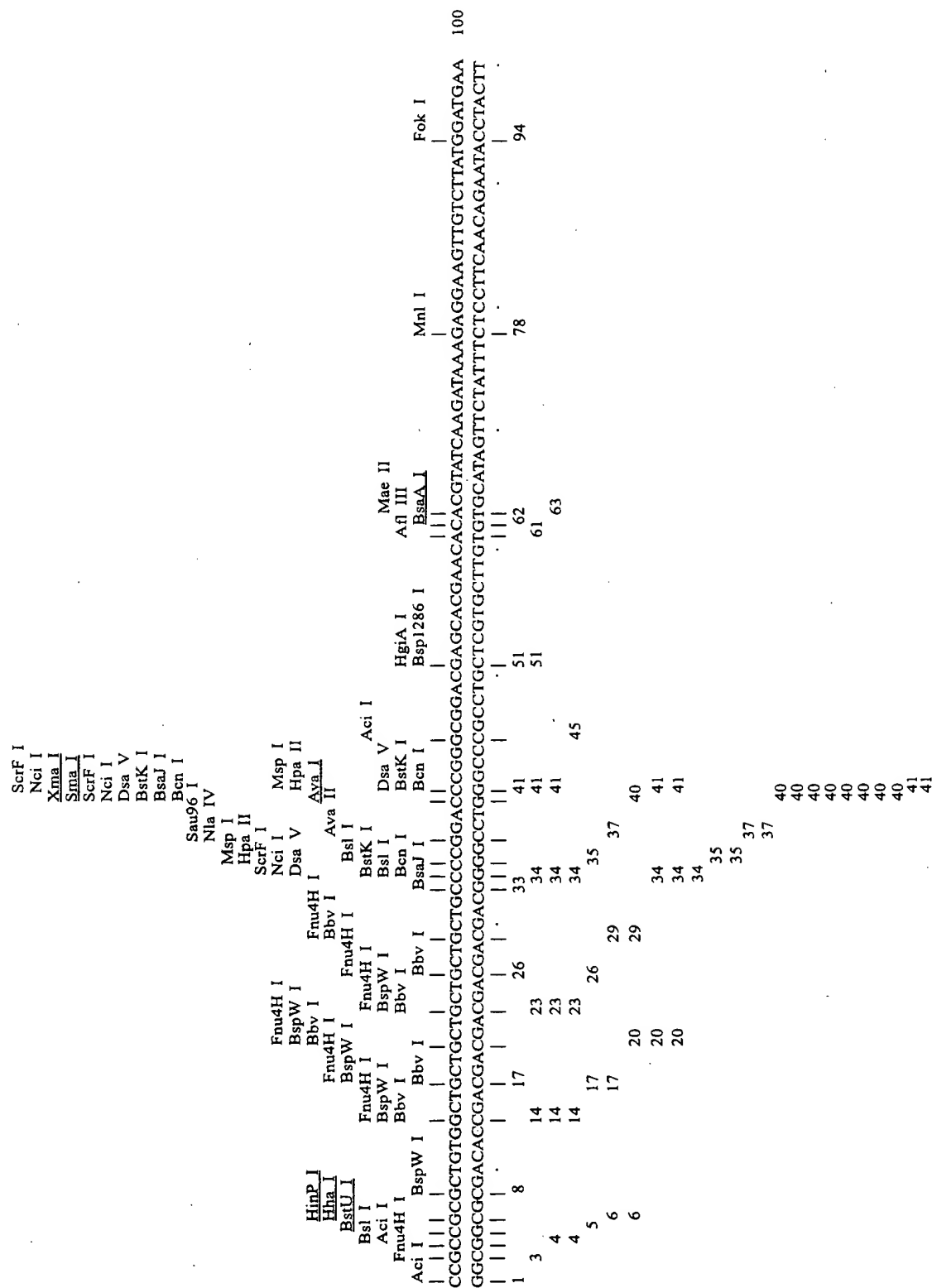
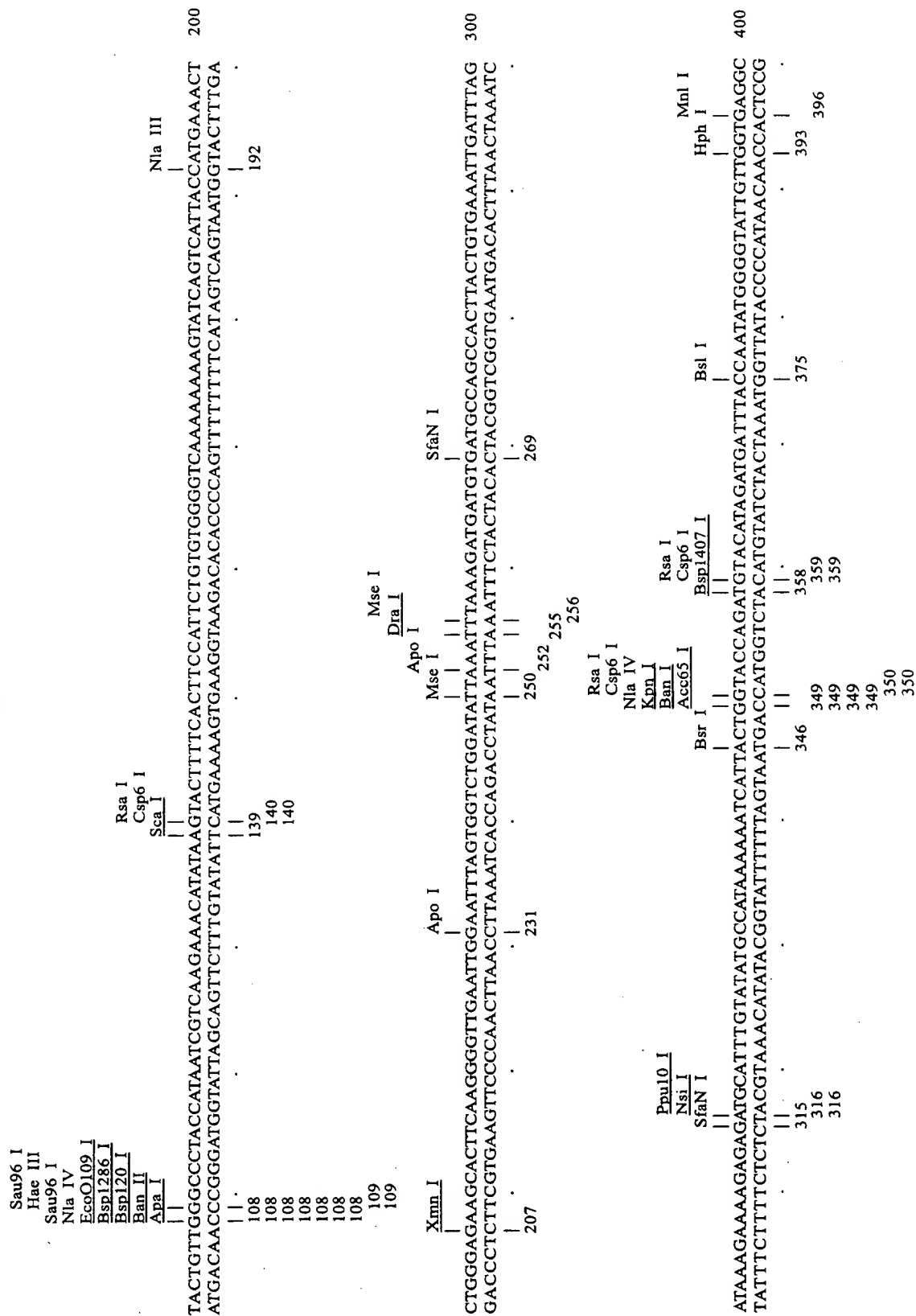


Fig. 19 B



BsaB I Sau96 I Mse I Taq I BsbB I Mse I Bfa I
 Mbo II Ava II
 414 430 457 467 477 481 489
 417 430

Bsr I Nla IV Apo I Dpn I Mbo I Dpn II Sau3A I Mbo I Dpn I Alw I
 Hph I 503 509 512 570 576 579 579 579 580 580 581

Sau3A I Mbo I Dpn I Alw I 600 600 600 600 600 600

Tfi I Hinf I Nla III BspH I BsaB I Hph I Mbo II Dpn II Dpn I Dde I Mse I
 623 623 652 653 656 659 662 662 662 677 693

ATCCGTCCTTTTTC AACATCGGATTCATTGGTTTTC AATTTTCA AACTCCTTCATGATGGTGATCTTCTTGGTGGGCTTAGTTTCAATGATTTTAATGAG 700
 TAGGCAGGAAAAAGTTGTAGCCTAAGTAACCAAAAAGTTAAAAAGTTGAGGAAGTACTACCACCTAGAAAGAACCCCGAATCAAAAGTTACTAAAAATTACTC

Fig. 19 D

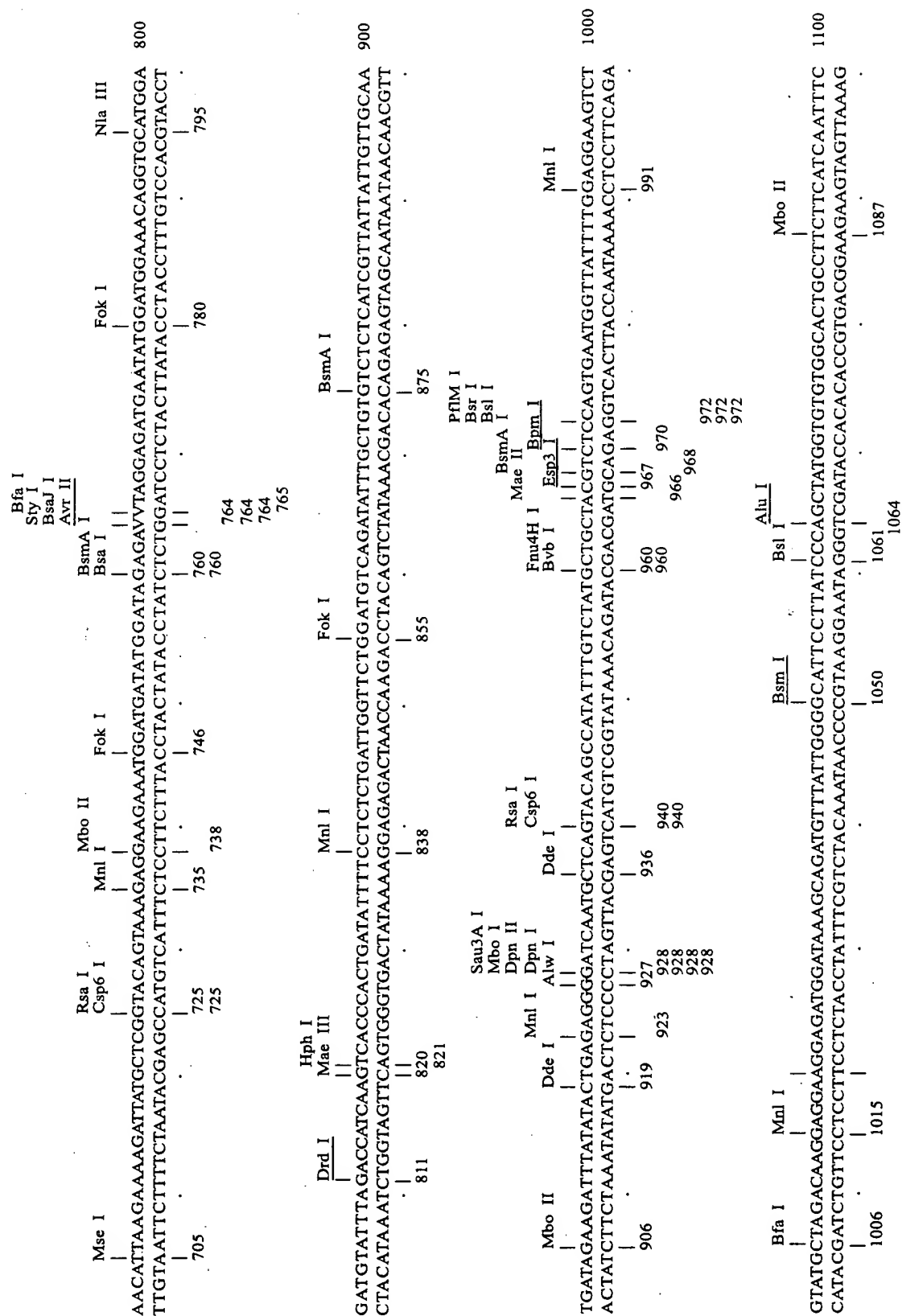
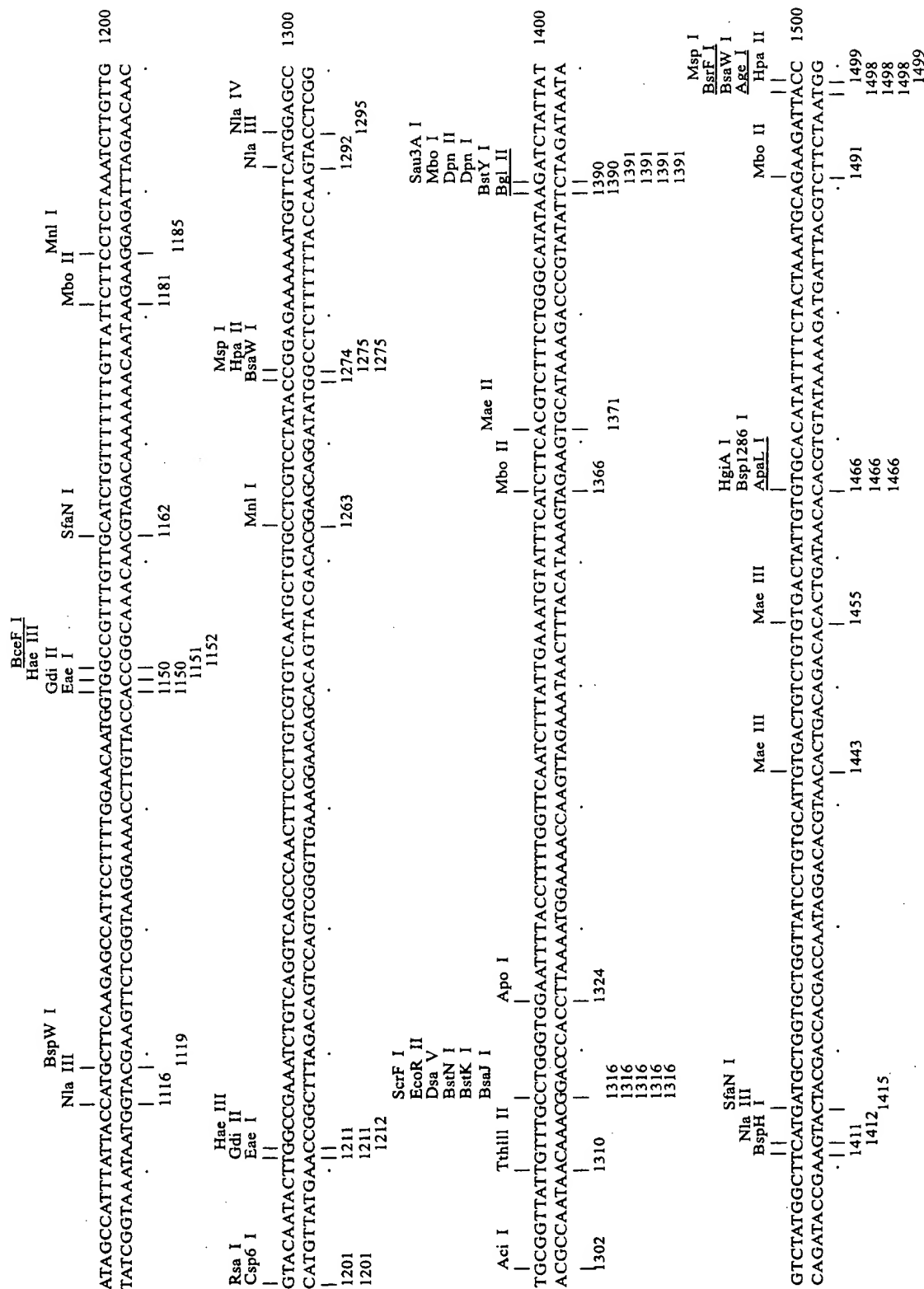


Fig. 19 E



[illegible]

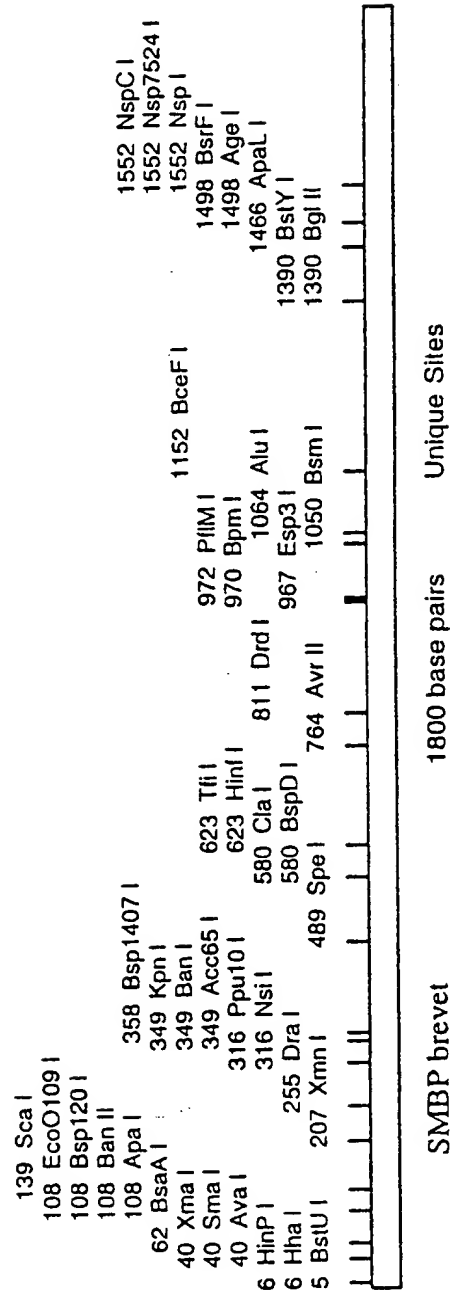


FIGURE 20

Enzyme	Site	<--	Pos.	-->
BstU I	cg/cg	4	5	1796
Hha I	gcg/c	5	6	1795
HinP I	g/cgc	5	6	1795
Ava I	c/ycgrg	39	40	1761
Sma I	ccc/ggg	39	40	1761
Xma I	c/ccggg	39	40	1761
BsaA I	yac/gtr	61	62	1739
Apa I	gggcc/c	107	108	1693
Ban II	grgcy/c	107	108	1693
Bsp120 I	g/ggccc	107	108	1693
EcoO109 I	rg/gnccy	107	108	1693
Sca I	agt/act	138	139	1662
Xmn I	gaann/nnttc	206	207	1594
Dra I	ttt/aaa	254	255	1546
Nsi I	atgca/t	315	316	1485
Ppu10 I	a/tgcat	315	316	1485
Acc65 I	g/gtacc	348	349	1452
Ban I	g/gyrcc	348	349	1452
Kpn I	ggtac/c	348	349	1452
Bsp1407 I	t/gtaca	357	358	1443
Spe I	a/ctagt	488	489	1312
BspD I	at/cgat	579	580	1221
Cla I	at/cgat	579	580	1221
Hinf I	g/antc	622	623	1178
Tfi I	g/awtc	622	623	1178
Avr II	c/ctagg	763	764	1037
Drd I	gacnnnn/nngtc	810	811	990
Esp3 I	cgctctc 1/5	966	967	834
Bpm I	ctggag 16/14	969	970	831
Pf1M I	ccannnn/ntgg	971	972	829
Bsm I	gaatgc 1/-1	1049	1050	751
Alu I	ag/ct	1063	1064	737
BceF I	acggc 12/13	1151	1152	649
Bgl II	a/gatct	1389	1390	411
BstY I	r/gatcy	1389	1390	411
ApaL I	g/tgcac	1465	1466	335
Age I	a/ccggt	1497	1498	303
BsrF I	r/ccggy	1497	1498	303
Nsp I	rcatg/y	1551	1552	249
Nsp7524 I	r/catgy	1551	1552	249
NspC I	rcatg/y	1551	1552	249

FIGURE 21

Fig. 22 A

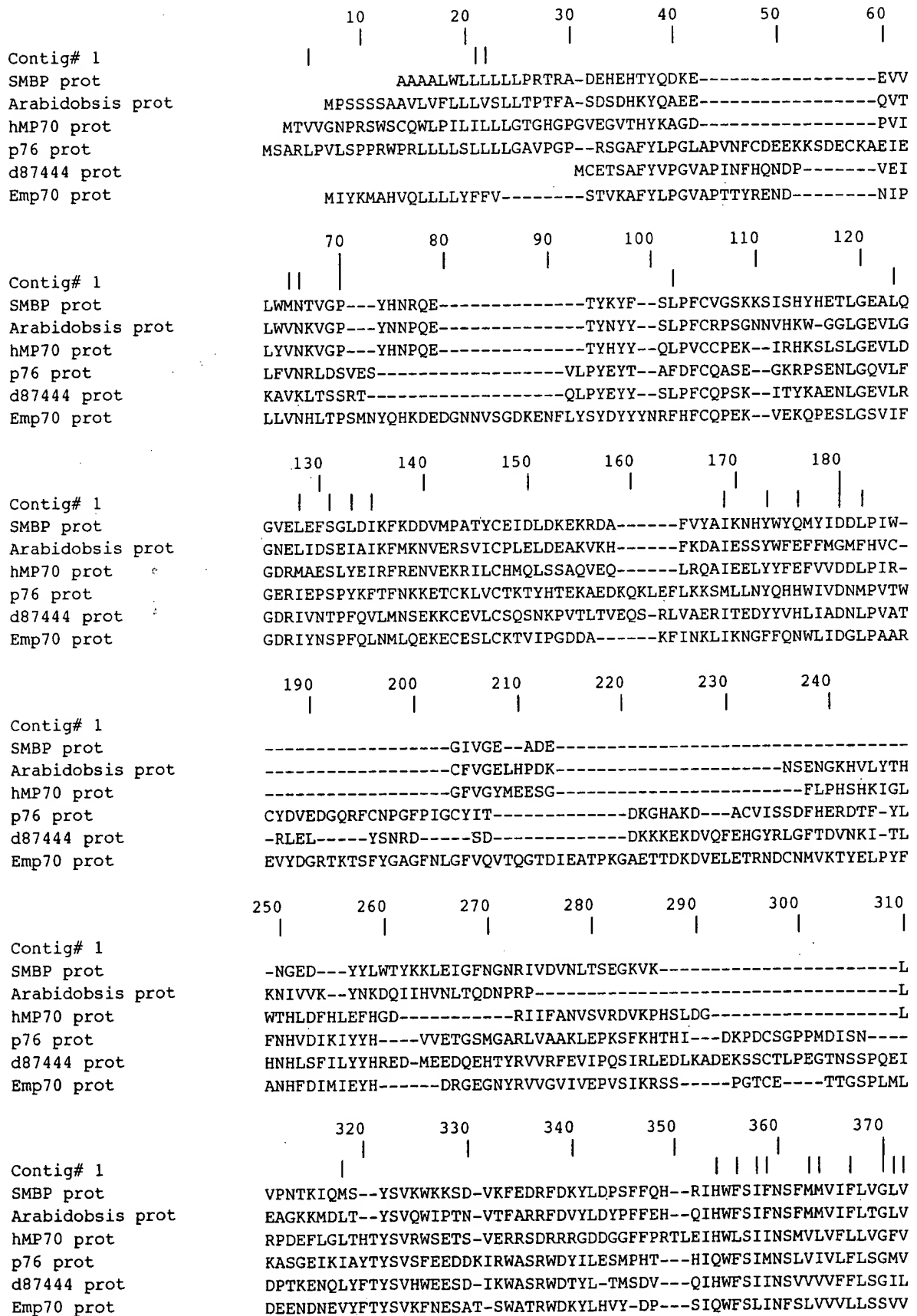


Fig. 22 B

Contig# 1
SMBP prot
Arabidopsis prot
hMP70 prot
p76 prot
d87444 prot
Emp70 prot

380 390 400 410 420 430

SMILMRTLRLKDYARTSKEEE-MDD-MDRDLGD-EYGWKQVHGDVFRPSSHPLIFSSSLIGSGC
SMILMRTLRLNDYAKYAREDDDLLES-LERDVSE-ESGWKLVHGDVFRPASSVLVLSAVVGTGA
AVILMRVLRNDLARYNLDEETTSAGSGDDDFDQGDNGWKIHTDVFRFPYRGLLCAVLGVGA
AMIMLRTLHKDIARYNQ-----MDSTED-AQEEFGWKLVHGDIFRPPRKGMLLSVFLGSGT
SMIIIRTLRKDIANYNK-----EDDIED-TMEESGWKLVHGDVFRPPQYOMILSSLLGSGI
IHSLRLALKSDFARYNE-----LNLDDD-FQEDSGWKLVHGDVFRSPSQSLTSLVVGSGV

Contig# 1
SMBP prot
Arabidopsis prot
hMP70 prot
p76 prot
d87444 prot
Emp70 prot

440 450 460 470 480 490

QIFAVSLIVIIIVAMIEDLYTER-GSMLSTAIFVYAATSPVNGYFGGSLYARQGGRRWIKQMF
QLALLVLLVILMAIVGTLVGR-GAIVTTFIVCYALTFSVSGYVSGGMYSRSGCKHWIKCMV
QFLALGTGIIVMALLGMFNVHRHGAISAAILLYALTCCISGYVSSHFYRQIGGERVWVNI
QILIMTFVTLEFACLGFLSPANRGALMTCVAVLVLLGTTPAGYVAARFYKSFGEKWKTNVL
QLFCMILIVIFVAMLGMLSPSSRGALMTTACFLFMGMGVFGGFSAGRLYRTLKGRHWKKGAF
QLFLMVTCSIFFAALGFLSPSSRGLATVMFILYALFGFVGSYTSMGYKFFNGPYWKANLI

Contig# 1
SMBP prot
Arabidopsis prot
hMP70 prot
p76 prot
d87444 prot
Emp70 prot

500 510 520 530 540 550

IGAFLIPAMVCGTAFFINFIAYYHASRAIPFGTMVAVCCICFFVILPLNLVGTILGRNLSC
LTASLFPFLFCFGIGFLLNTIAIFYGSLAAIPFGTMVVVFIWGFISFPLALLGTVVGRNWSG
LTTSLFSVPFFLTWSVNVSVHWANGSTQALPATTILLLLTVWLLVGFPLTVIGGIFGKNNAS
LTSFLCPGIVFADFFIMNLILWGESSAAIPFGTLVAILALWFICISVPLTFIGAYFGFKK-N
CTATLYPGVVFEGICFVLNCFIWKHSSGAVPFFPTMVALLCMWFGISLPLVYLGYFFGFRK-Q
LTPLLVPGAILLIILNFFLMFVHSSGVIPASTLFFMVFLWFLFSIPSSFAGSLIARKRCH

Contig# 1
SMBP prot
Arabidopsis prot
hMP70 prot
p76 prot
d87444 prot
Emp70 prot

560 570 580 590 600 610 620

QPNFPCRVNAVPRPIPEKKWFMEPAVIVCLGGILPFGSIFIEMYFIFTSFWAYKIYYVYGFM
APNNPCRVKTIPRPIPEKKWYLTSPVSVSLMGGLLPFGSIFIEMYFVFTSFWNKYVYYVYGFM
PFDAPCRTKNIAREINPQWPYKSTDIHMTVGGFLPFSAISVELYYIFATVWGREQYTLYGIL
AIEHPVRTNQIPRQIPEQSFYTKPLPGIIMGGILPFGCIFQLFIFILNSIWSHQMYMFGFL
PYDNPVRTNQIPRQIPEQRWYMNRFVGLMAGILPFGAMFIELFFIFSAIWENQFYFLFGFL
WDEHPTKTNQIARQIPFPWYLTIPATLIAGIFPFGSIAVELYFIYTSLWFNKIFYMFGFL

Contig# 1
SMBP prot
Arabidopsis prot
hMP70 prot
p76 prot
d87444 prot
Emp70 prot

630 640 650 660 670 680

MLVLVILCIVTVCTIVCTYFLLNAEDYRWQWTSFLSAAST-AIYVYMYSFYYYFFKTKMYG
LLVFVILVIVTVCTIVGTYFLLNAENYHWQWTSFFSAAST-AVYVYLYSIYYYVVKTKMSG
FFVFALLSVGASISIALTYFQLSGEDYRWWRSVLSVGST-GLFIFLYSVFYARRSNMSG
FLVFILVITCSEATILLCYFHLCAEDYHWQWRSFLTSGFT-AVYFLIYAVHYFFSKLQITG
FLVFILVVSQSQISIVMVYFQLCAEDYRWWRNFLVSGGS-AFYVLVYAIIFYVKNLDIVE
FFSFLLLTLTSSLVTLITYHSLCLENWKWQWRGFIIGGAGCALYVFIHSILF--TKFKLGG

Contig# 1
SMBP prot
Arabidopsis prot
hMP70 prot
p76 prot
d87444 prot
Emp70 prot

690 700 710 720

LFQTSFYFGYMAVFSTALGIMCGAIGMGTSAFVRKIYTNVKID
FFQTSFYFGYTMMFCLGLGILCGAVGYLGSNLFVRRIYRNKCD
AVQTVEFFGYSLLTGYVFFLMLGTISFFSSLKFIYIYVNLKMD
TASTILYFGYTMIMVLIFLFTGTIGFFACFWFVKIYSVVKVD
FIPSLLYFGYTALMVLFSWLLTGTIGFYAAYMFVRKIYAAVKID
FTTIVLYVGYSSVISLLCCLVTGSIGFISSMLFVRKIYSSIKVD

Fig. 23 A

Hydropathy index (Kyte-Doolittle, 1982)

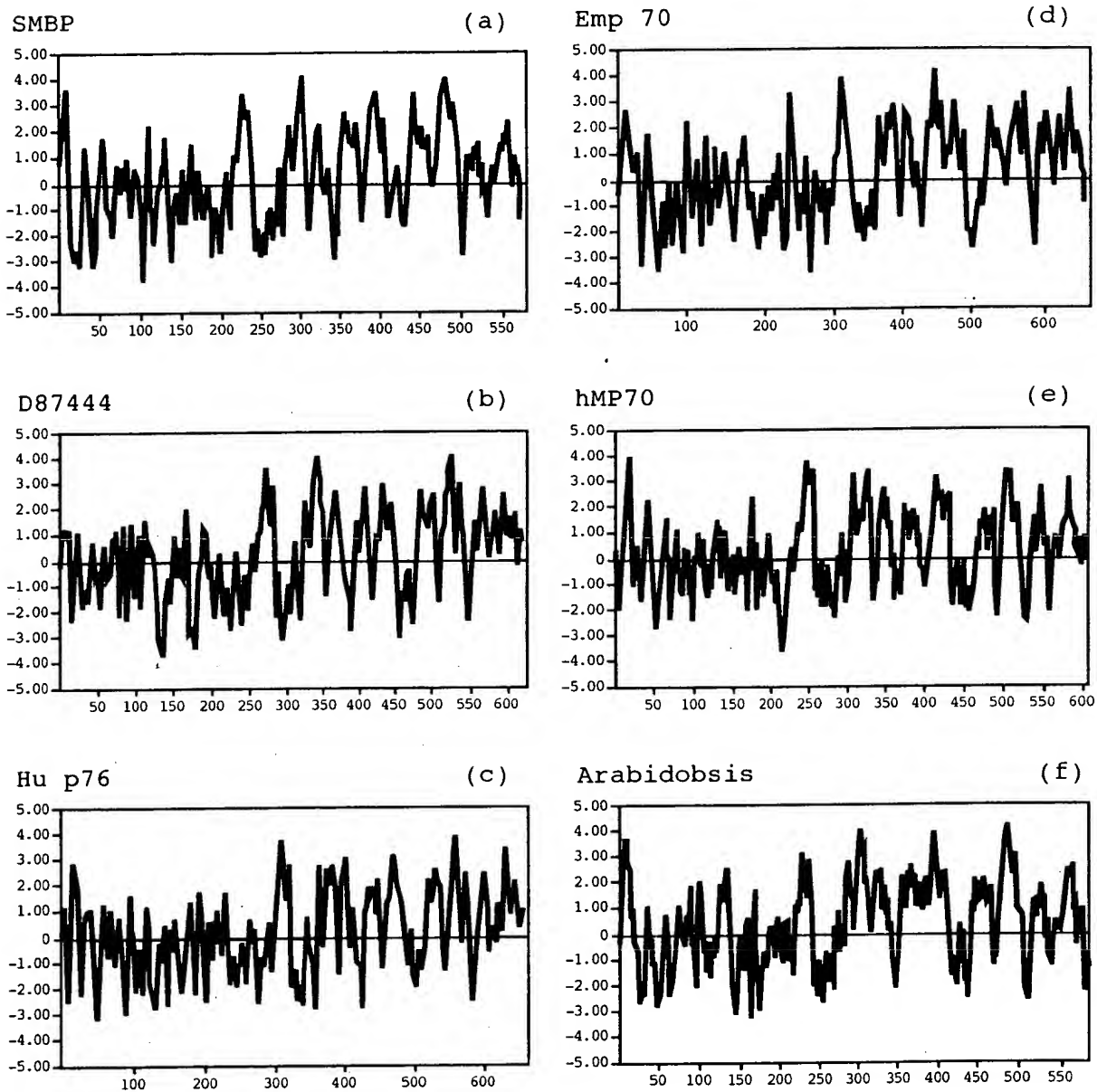
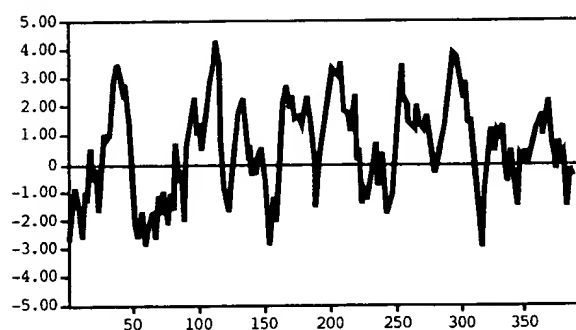


Fig. 23 B

Hydropathy index (Kyte-Doolittle, 1982)

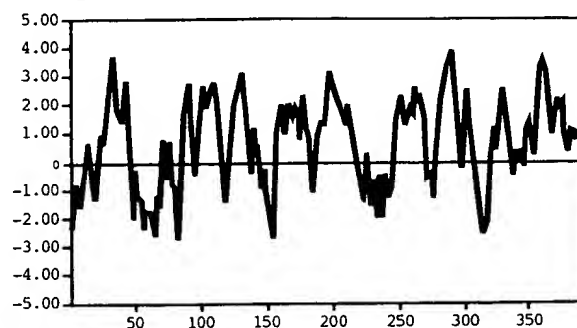
SMBP

(a)



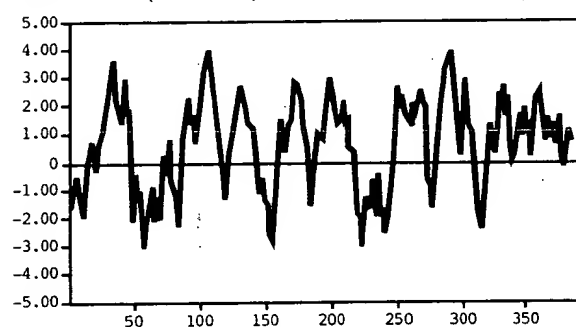
Hu p76 (C-ter)

(c)



D87444 (C-ter)

(b)



Emp 70 (C-ter)

(d)

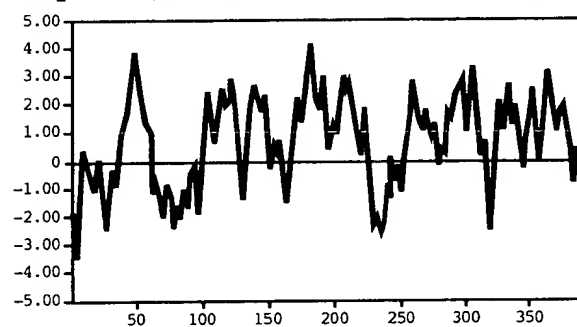


Fig. 24 A

1 CC GCC GCG CTG TGG CTG CTG CTG CTG CTG CCC CGG ACC CGG GCG GAC GAG CAC GAA CAC ACG TAT CAA GAT 74
1 A A L W L L L L L L L P R T R A D E H E H T Y Q D 24

75 AAA GAG GAA GTT GTC TTA TGG ATG AAT ACT GTT GGG CCC TAC CAT AAT CGT CAA GAA ACA TAT CCG TAC TTT TCA CTT CCA TTC TGT GTG 164
25 K E E V V L W M N T V G P Y H N R Q E T Y K Y F S L P F C V 54

165 GGG TCA AAA AAA AGT ATC AGT CAT TAC CAT GAA ACT CTG GGA GAA GCA CTT CAA GGG GTT GAA TTG GAA TTT AGT GGT CTG GAT ATT AAA 254
55 G S K K S I S H Y H E T L G E A L Q G V E L E F S G L D I K 84

255 TTT AAA GAT GAT GTG ATG CCA GCC ACT TAC TGT GAA ATT GAT TTA GAT AAA GAA AAG AGA GAT GCA TTT GTA TAT CCC ATA AAA AAT CAT 344
85 F K D D V M P A T Y C E I D L D K E K R D A F V Y A I K N H 114

345 TAC TGG TAC CAG ATG TAC ATA GAT GAT TTA CCA ATA TGG GGT ATT GTT GGT GAG GCT GAT GAA AAT GGA GAA GAT TAC TAT CTT TGG ACC 434
115 Y W Y Q M Y I D D L P I W G I V G E A D E N G E D Y Y L W T 144

435 TAT AAA AAA CTT GAA ATA GGT TTT AAT GGA AAT CGA ATT GTT GAT GTT AAT CTA ACT AGT GAA GGA AAG GTG AAA CTG CTT CCA AAT ACT 524
145 Y K K L E I G F N G N R I V D V N L T S E G K V K L V P N T 174

525 AAA ATC CAG ATG TCA TAT TCA GTA AAA TGG AAA AAC TCA GAT GTG AAA TTT GAA GAT CGA TTT GAC AAA TAT CTT GAT CCG TCC TTT TTT 614
175 K I Q M S Y S V R W K K S D V K F E D R F D K Y L D P S F F 204

615 CAA CAT CGG ATT CAT TGG TTT TCA ATT TTC AAC TCC TTC ATG ATG GTG ATC TTC TTG GTG GGC TTA GTT TCA ATG ATT TTA ATG AGA ACA 704
205 Q E R I H W F S I F N S F M M V I F L V G L V S M I L M R T 234

705 TTA AGA AAA GAT TAT GCT CGG TAC AGT AAA GAG GAA GAA ATG GAT GAT ATG GAT AGA GAC CTA GGA GAT GAA TAT GGA TGG AAA CAG GTG 794
235 L R K D Y A R Y S K E E E M D D M D R D L G D E Y G W K Q V 264

795 CAT GGA GAT GTA TTT AGA CCA TCA AGT CAC CCA CTG ATA TTT TCC TCT CTG ATT GGT TCT GGA TGT CAG ATA TTT GCT GTG TCT CTC ATC 884
265 H G D V F R P S S H P L I F S S L I G S G C Q I F A V S L I 294

885 GTT ATT ATT GTT GCA ATG ATA GAA GAT TTA TAT ACT GAG ACG GGA TCA ATG CTC AGT ACA GCC ATA TTT GTC TAT GCT GCT ACG TCT CCA 974
295 V I I V A M I E D L Y T E R G S M L S T A I F V Y A A T S P 324

975 GTG AAT GGT TAT TTT GGA GGA AGT CTG TAT GCT AGA CAA GGA GGA AGG AGA TGG ATA AAG CAG ATG TTT ATT GGG GCA TTC CTT ATC CCA 1064
325 V N G Y F G G S L Y A R Q G G R R W I K Q M F I G A F L I P 354

1065 CCT ATG GTG TGT GGC ACT GCC TTC TTC ATC AAT TTC ATA GCC ATT TAT TAC CAT GCT TCA AGA GCC ATT CCT TTT GGA ACA ATG GTG GCC 1154
355 A M V C G T A F F I N F I A I Y Y H A S R A I P F G T M V A 384

1155 GTT TGT TGC ATC TGT TTT TTT GTT ATT CTT CCT CTA AAT CTT GTT GGT ACA ATA CTT GGC CGA AAT CTG TCA GGT CAG CCC AAC TTT CCT 1244
385 V C C I C F F V I L P L N L V G T I L G R N L S G Q P N F P 414

1245 TGT GGT GTC AAT GCT GTG CCT CGT CCT ATA CCG GAG AAA AAA TGG TTC ATG GAG CCT GCG GTT ATT GTT TGC CTG GGT GGA ATT TTA CCT 1334
415 C R V N A V P R P I P E K K W F M E P A V I V C L G G I L P 444

1335 TTT GGT TCA ATC TTT ATT GAA ATG TAT TTC ATC TTC ACG TCT TTC TGG GCA TAT AAG ATC TAT TAT GTC TAT GGC TTC ATG ATG CTG GTG 1424
445 F G S I F I E M Y F I F T S F W A Y K I Y Y V Y G F M M L V 474

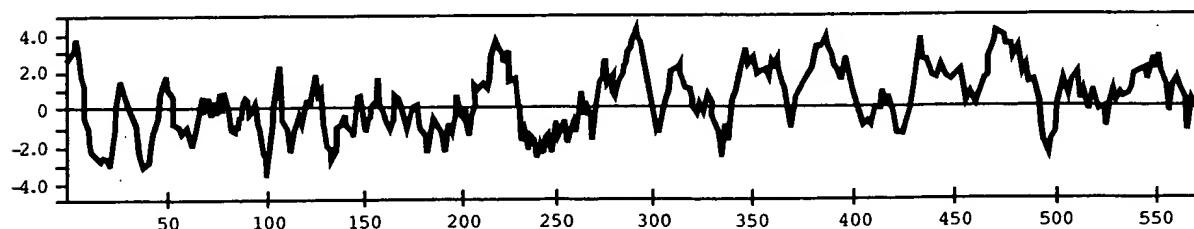
1425 CTG GTT ATC CTG TGC ATT GTG ACT GTC TGT GTG ACT ATT GTG TGC ACA TAT TTT CTA CTA AAT GCA GAA GAT TAC CGG TGG CAA TGG ACA 1514
475 L V I L C I V T V C V T I V C T Y F L L N A E D Y R W Q W T 504

1515 AGT TTT CTC TCT GCT GCA TCA ACT GCA ATC TAT GTT TAC ATG TAT TCC TTT TAC TAC TAT TTT TTC AAA ACA AAG ATG TAT GGC TTA TTT 1604
505 S F L S A A S T A I Y V Y M Y S F Y Y Y F F K T K M Y G L F 534

1605 CAA ACA TCA TTT TAC TTT GGA TAT ATG CCG GTA TTT AGC ACA GCC TTG GGG ATA ATG TGT GGA GCG ATT GGT TAC ATG GGA ACA AGT TTT 1694
535 Q T S F Y F G Y M A V F S T A L G I M C G A I G Y M G T S A 564

1695 TTT GTC CGA AAA ATC TAT ACT AAT CTG AAA ATT GAC TAG AGACCCAAGAAAACCTGGAACCTTGGATCAATTTCTTTTCATAGGGGTGGAACCTGCACAGCAAAA 1800
565 F V R K I Y T N V K I D 576

Fig. 24 B



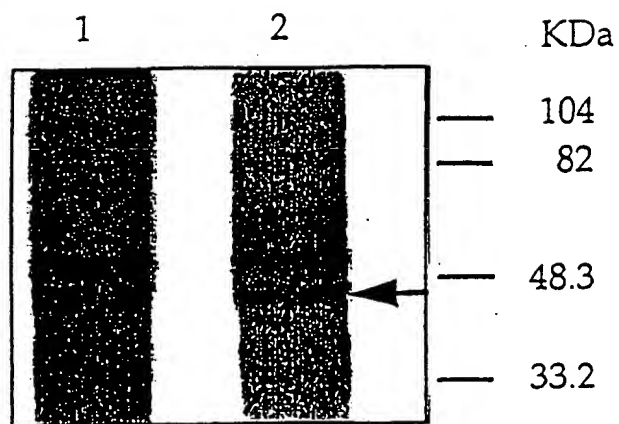


FIGURE 25

BEST AVAILABLE COPY